

10/25#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/945,326

DATE: 09/20/2001

TIME: 13:49:51

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09202001\I945326.raw

ENTERED

4 <110> APPLICANT: Meyers, Rachel
 5 Hunter, John Joseph
 7 <120> TITLE OF INVENTION: 62112, A NOVEL HUMAN DEHYDROGENASE AND
 8 USES THEREOF
 10 <130> FILE REFERENCE: MNI-187
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/945,326
 C--> 12 <141> CURRENT FILING DATE: 2001-08-31
 12 <150> PRIOR APPLICATION NUMBER: 60/229,831
 13 <151> PRIOR FILING DATE: 2000-08-31
 15 <160> NUMBER OF SEQ ID NOS: 3
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2452
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (67)...(1932)
 28 <400> SEQUENCE: 1
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 30 ggcAGC atg agc ggc tgc ggg ctc ttc ctg cgc acc acg gct gcg gct 108
 31 Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala
 32 1 5 10
 34 cgt gcc tgc cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg 156
 35 Arg Ala Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu
 36 15 20 25 30
 38 cgc acc agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc 204
 39 Arg Thr Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly
 40 35 40 45
 42 aaa atc aag aag aaa gaa gtt ttc cca ttt cca gaa gtt agc caa gat 252
 43 Lys Ile Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp
 44 50 55 60
 46 gaa ctt aat gaa atc aat cag ttc ttg gga ccc gtg gaa aaa ttc ttc 300
 47 Glu Leu Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe.
 48 65 70 75
 50 act gaa gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca 348
 51 Thr Glu Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro
 52 80 85 90
 54 gat gaa act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa 396
 55 Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln
 56 95 100 105 110
 58 gtc cca gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca 444
 59 Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser
 60 115 120 125
 62 aga cta ggg gag atc atc agc atg gat ggg tcc atc act gtg acc ctg 492
 63 Arg Leu Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu
 64 130 135 140

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66	gca	gcg	cac	cag	gct	att	ggc	ctc	aag	ggg	atc	atc	ttg	gct	ggc	act	540
67	Ala	Ala	His	Gln	Ala	Ile	Gly	Leu	Lys	Gly	Ile	Ile	Leu	Ala	Gly	Thr	
68						145					150					155	
70	gag	gag	cag	aaa	gcc	aaa	tac	ttg	cct	aaa	ctg	gct	tcc	ggg	gag	cac	588
71	Glu	Glu	Gln	Lys	Ala	Lys	Tyr	Leu	Pro	Lys	Leu	Ala	Ser	Gly	Glu	His	
72						160					165					170	
74	att	gca	gcc	ttc	tgc	ctc	acg	gag	cca	gcc	agt	ggg	agc	gat	gca	gcc	636
75	Ile	Ala	Ala	Phe	Cys	Leu	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Asp	Ala	Ala	
76	175						180				185					190	
78	tca	atc	cg	agc	aga	gcc	aca	cta	agt	gaa	gac	aag	aag	cac	tac	atc	684
79	Ser	Ile	Arg	Ser	Arg	Ala	Thr	Leu	Ser	Glu	Asp	Lys	Lys	His	Tyr	Ile	
80						195				200					205		
82	ctc	aat	ggc	tcc	aag	gtc	tgg	att	act	aat	gga	gga	ctg	gcc	aat	att	732
83	Leu	Asn	Gly	Ser	Lys	Val	Trp	Ile	Thr	Asn	Gly	Gly	Leu	Ala	Asn	Ile	
84						210				215					220		
86	ttt	act	gtg	ttt	gca	aag	act	gag	gtc	gtt	gat	tct	gat	gga	tca	gtg	780
87	Phe	Thr	Val	Phe	Ala	Lys	Thr	Glu	Val	Val	Asp	Ser	Asp	Gly	Ser	Val	
88						225				230					235		
90	aaa	gac	aaa	atc	aca	gca	ttc	ata	gta	gaa	aga	gac	ttt	ggt	gga	gtc	828
91	Lys	Asp	Lys	Ile	Thr	Ala	Phe	Ile	Val	Glu	Arg	Asp	Phe	Gly	Gly	Val	
92	240						245				250						
94	act	aat	ggg	aaa	ccc	gaa	gat	aaa	tta	ggc	att	cg	ggc	tcc	aac	act	876
95	Thr	Asn	Gly	Lys	Pro	Glu	Asp	Lys	Leu	Gly	Ile	Arg	Gly	Ser	Asn	Thr	
96	255					260				265					270		
98	tgt	gaa	gtc	cat	ttt	gaa	aac	acc	aag	ata	cct	gtg	gaa	aac	atc	ctt	924
99	Cys	Glu	Val	His	Phe	Glu	Asn	Thr	Lys	Ile	Pro	Val	Glu	Asn	Ile	Leu	
100						275				280					285		
102	gga	gag	gtc	gga	gat	ggg	ttt	aag	gt	gcc	atg	aac	atc	ctc	aac	agc	972
103	Gly	Glu	Val	Gly	Asp	Gly	Phe	Lys	Val	Ala	Met	Asn	Ile	Leu	Asn	Ser	
104						290				295					300		
106	ggc	cgg	ttc	agc	atg	ggc	agc	gtc	gt	gct	ggg	ctg	ctc	aag	aga	ttg	1020
107	Gly	Arg	Phe	Ser	Met	Gly	Ser	Val	Val	Ala	Gly	Leu	Leu	Lys	Arg	Leu	
108						305				310					315		
110	att	gaa	atg	act	gt	gag	tac	gcc	tgc	aca	agg	aaa	cag	ttt	aac	aag	1068
111	Ile	Glu	Met	Thr	Ala	Glu	Tyr	Ala	Cys	Thr	Arg	Lys	Gln	Phe	Asn	Lys	
112						320				325					330		
114	agg	ctc	agt	gaa	ttt	gga	ttg	att	cag	gag	aaa	ttt	gca	ctg	atg	gct	1116
115	Arg	Leu	Ser	Glu	Phe	Gly	Leu	Ile	Gln	Glu	Lys	Phe	Ala	Leu	Met	Ala	
116	335						340				345					350	
118	cag	aag	gct	tac	gtc	atg	gag	agt	atg	acc	tac	ctc	aca	gca	ggg	atg	1164
119	Gln	Lys	Ala	Tyr	Val	Met	Glu	Ser	Met	Thr	Tyr	Leu	Thr	Ala	Gly	Met	
120						355				360					365		
122	ctg	gac	caa	cct	ggc	ttt	ccc	gac	tgc	tcc	atc	gag	gca	gcc	atg	gt	1212
123	Leu	Asp	Gln	Pro	Gly	Phe	Pro	Asp	Cys	Ser	Ile	Glu	Ala	Ala	Met	Val	
124						370				375					380		
126	aag	gt	t	tc	agc	tcc	g	g	cc	g	tt	c	tg	tg	at	g	1260
127	Lys	Val	Phe	Ser	Ser	Glu	Ala	Ala	Trp	Gln	Cys	Val	Ser	Glu	Ala	Leu	
128						385				390					395		
130	cag	atc	ctc	ggg	ggc	ttg	ggc	tac	aca	agg	gac	tat	ccg	tac	gag	cgc	1308

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131 Gln Ile Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg			
132 400	405	410	
134 ata ctg cgt gac acc cgc atc ctc ctc atc ttc gag gga acc aat gag			1356
135 Ile Leu Arg Asp Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn Glu			
136 415	420	425	430
138 att ctc cgg atg tac atc gcc ctg acg ggt ctg cag cat gcc ggc cgc			1404
139 Ile Leu Arg Met Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly Arg			
140 435	440	445	
142 atc ctg act acc agg atc cat gag ctt aaa cag gcc aaa gtg agc aca			1452
143 Ile Leu Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr			
144 450	455	460	
146 gtc atg gat acc gtt ggc cgg agg ctt cgg gac tcc ctg ggc cga act			1500
147 Val Met Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr			
148 465	470	475	
150 gtg gac ctg ggg ctg aca ggc aac cat gga gtt gtg cac ccc agt ctt			1548
151 Val Asp Leu Gly Leu Thr Gly Asn His Gly Val Val His Pro Ser Leu			
152 480	485	490	
154 gcg gac agt gcc aac aag ttt gag gag aac acc tac tgc ttc ggc cgg			1596
155 Ala Asp Ser Ala Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly Arg			
156 495	500	505	510
158 acc gtg gag aca ctg ctg ctc cgc ttt ggc aag acc atc atg gag gag			1644
159 Thr Val Glu Thr Leu Leu Arg Phe Gly Lys Thr Ile Met Glu Glu			
160 515	520	525	
162 cag ctg gta ctg aag cgg gtg gcc aac atc ctc atc aac ctg tat ggc			1692
163 Gln Leu Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly			
164 530	535	540	
166 atg acg gcc gtg ctg tcg cgg gcc agc cgc tcc atc cgc att ggg ctc			1740
167 Met Thr Ala Val Leu Ser Arg Ala Ser Arg Ser Ile Arg Ile Gly Leu			
168 545	550	555	
170 cgc aac cac gac cac gag gtt ctc ttg gcc aac acc ttc tgc gtg gaa			1788
171 Arg Asn His Asp His Glu Val Leu Leu Ala Asn Thr Phe Cys Val Glu			
172 560	565	570	
174 gct tac ttg cag aat ctc ttc agc ctc tct cag ctg gac aag tat gct			1836
175 Ala Tyr Leu Gln Asn Leu Phe Ser Leu Ser Gln Leu Asp Lys Tyr Ala			
176 575	580	585	590
178 cca gaa aac cta gat gag cag att aag aaa gtg tcc cag cag atc ctt			1884
179 Pro Glu Asn Leu Asp Glu Gln Ile Lys Lys Val Ser Gln Gln Ile Leu			
180 595	600	605	
182 gag aag cga gcc tat atc tgt gcc cac cct ctg gac agg aca tgc tga			1932
183 Glu Lys Arg Ala Tyr Ile Cys Ala His Pro Leu Asp Arg Thr Cys *			
184 610	615	620	
186 ggcaggggac agtgtccccct gctaccgccc gcccctaccc atggcccggt gctggatgac			1992
187 tgttactctt ttttcaagaag gtgttggat tatcacaggt taagcctttt gttccccgtc			2052
188 tgcacctgaa ggggtgtcgc ctggcctggg agagcctttt ccaggtttt acctgcaggc			2112
189 agtgctctct aacaggacca tcacagcttc tgaactgagc cggagagaga gaatggaatt			2172
190 gctgaccctt ggaactggcg ggtattctgg tcattgagga gacaccatag tggaaactgg			2232
191 ggcttatgtc gctgcctcca ggggtgtgagg tgggtgggaa cctgtgtca ggtgtggatag			2292
192 ccatttctgc tcaaccacac attctctaag aaacagctt aagactctgt ctgggtcatt			2352
193 catttaaact agaagcagag gcactaaaa catgtaccag gaaccattta acaaagaata			2412

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194 taaaatgtca caatctgtgt actgttaaaa aaaaaaaaaaa 2452
 196 <210> SEQ ID NO: 2
 197 <211> LENGTH: 621
 198 <212> TYPE: PRT
 199 <213> ORGANISM: Homo sapiens
 201 <400> SEQUENCE: 2
 202 Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
 203 1 5 10 15
 204 Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
 205 20 25 30
 206 Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
 207 35 40 45
 208 Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu
 209 50 55 60
 210 Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu
 211 65 70 75 80
 212 Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu
 213 85 90 95
 214 Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro
 215 100 105 110
 216 Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu
 217 115 120 125
 218 Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala
 219 130 135 140
 220 His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu
 221 145 150 155 160
 222 Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala
 223 165 170 175
 224 Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile
 225 180 185 190
 226 Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn
 227 195 200 205
 228 Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr
 229 210 215 220
 230 Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp
 231 225 230 235 240
 232 Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn
 233 245 250 255
 234 Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu
 235 260 265 270
 236 Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu
 237 275 280 285
 238 Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg
 239 290 295 300
 240 Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu
 241 305 310 315 320
 242 Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu
 243 325 330 335
 244 Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala Gln Lys

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245	340	345	350
246 Ala	Tyr Val	Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met Leu Asp	
247	355	360	365
248 Gln Pro	Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met Val Lys Val		
249	370	375	380
250 Phe Ser	Ser Glu Ala Ala Trp Gln Cys Val Ser Glu Ala Leu Gln Ile		
251	385	390	395
252 Leu Gly	Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg Ile Leu		400
253	405	410	415
254 Arg Asp	Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn Glu Ile Leu		
255	420	425	430
256 Arg Met	Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly Arg Ile Leu		
257	435	440	445
258 Thr Thr	Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr Val Met		
259	450	455	460
260 Asp Thr	Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr Val Asp		
261	465	470	475
262 Leu Gly	Leu Thr Gly Asn His Gly Val Val His Pro Ser Leu Ala Asp		480
263	485	490	495
264 Ser Ala	Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly Arg Thr Val		
265	500	505	510
266 Glu Thr	Leu Leu Leu Arg Phe Gly Lys Thr Ile Met Glu Glu Gln Leu		
267	515	520	525
268 Val Leu	Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly Met Thr		
269	530	535	540
270 Ala Val	Leu Ser Arg Ala Ser Arg Ser Ile Arg Ile Gly Leu Arg Asn		
271	545	550	555
272 His Asp	His Glu Val Leu Leu Ala Asn Thr Phe Cys Val Glu Ala Tyr		560
273	565	570	575
274 Leu Gln	Asn Leu Phe Ser Leu Ser Gln Leu Asp Lys Tyr Ala Pro Glu		
275	580	585	590
276 Asn Leu	Asp Glu Gln Ile Lys Lys Val Ser Gln Gln Ile Leu Glu Lys		
277	595	600	605
278 Arg Ala	Tyr Ile Cys Ala His Pro Leu Asp Arg Thr Cys		
279	610	615	620
282 <210>	SEQ ID NO: 3		
283 <211>	LENGTH: 1863		
284 <212>	TYPE: DNA		
285 <213>	ORGANISM: Homo sapiens		
287 <220>	FEATURE:		
288 <221>	NAME/KEY: CDS		
289 <222>	LOCATION: (1)...(1863)		
291 <400>	SEQUENCE: 3		
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293 Met	Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala		
294 1	5	10	15
296 tgc	cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg cgc acc	96	
297 Cys Arg	Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr		
298	20	25	30

VERIFICATION SUMMARY

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Output Set: N:\CRF3\09202001\I945326.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date